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(54) Title: METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL EFFICIENCY OF A CODON

(57) Abstract

A method is disclosed for determining the translational efficiency of an individual codon in a cell. The method comprises introducing into the cell a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of said individual codon, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide and measuring expression of said reporter protein in said cell to determine the translational efficiency of said codon.

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METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL EFFICIENCY OF A CODON

FIELD OF THE INVENTION

THIS INVENTION relates generally to gene expression and in particular, to a method and polynucleotides for determining codon utilization in particular cells or tissues of an organism. More particularly, the method and polynucleotides of the invention are concerned with ascertaining codon preferences in cells or tissues for the purpose of modifying the translational efficiency of protein-encoding polynucleotides in those cells or tissues.

BACKGROUND OF THE INVENTION

It is well known that a "triplet" codon of four possible nucleotide bases can exist in 64 variant forms. These forms provide the message for only 20 different amino acids (as well as translation initiation and termination) and this means that some amino acids can be encoded by more than one codon. Some amino acids have as many as six "redundant", alternative codons while some others have a single, required codon.

For reasons not completely understood, codon utilization is highly biased in that alternative codons are not at all uniformly present in the endogenous DNA of differing cell types. In this regard, there appears to exist a variable natural hierarchy of "preference" for certain codons between different cell types or between different organisms.

Codon usage patterns have been shown to correlate with relative abundance of isoaccepting transfer RNA (iso-tRNA) species, and with genes encoding proteins of high versus low abundance. Moreover, the present inventors recently

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discovered that the intracellular abundance of different iso-
tRNAs varies in different cells or tissues of a single multi-
cellular organism (see copending International Application
No. PCT/AU98/00530).

5   The implications of codon preference phenomena on gene
expression are manifest in that these phenomena can affect
the translational efficiency of messenger RNA (mRNA). It is
widely known in this regard that translation of "rare
codons", for which the corresponding iso-tRNA is in
10   relatively low abundance, may cause a ribosome to pause
during translation which can lead to a failure to complete a
nascent polypeptide chain and an uncoupling of transcription
and translation.

         A primary goal in recombinant research is to provide
15   transgenic organisms with expression of a foreign gene in an
amount sufficient to confer the desired phenotype to the
organism. However, expression of the foreign gene may be
severely impeded if a particular host cell of the organism or
the organism itself has a low abundance of iso-tRNAs
20   corresponding to one or more codons of the foreign gene.
Accordingly, a major aim of investigators in this field is to
first ascertain the codon preference for particular cells or
tissues in which a foreign gene is to be expressed, and to
subsequently alter the codon composition of the foreign gene
25   for optimized expression in those cells or tissues.

         Codon preference may be determined simply by analyzing
the frequency at which codons are used by genes expressed in
a particular cell or tissue or in a plurality of cells or
tissues of a given organism. Codon frequency tables as well
30   as suitable methods for determining frequency of codon usage
in an organism are described, for example, in an article by
Sharp *et al* (1988, *Nucleic Acids Res.* **16** 8207-8211). The
relative level of gene expression (*e.g.*, detectable protein
expression Vs no detectable protein expression) can provide

an indirect measure of the relative abundance of specific iso-tRNAs expressed in different cells or tissues.

Alternatively, codon preference may be determined by measuring the relative intracellular abundance of different iso-tRNA species. For example, reference may be made to copending International Application No. PCT/AU98/00530 that describes a method that utilizes labeled oligonucleotides specific for different iso-tRNAs to probe an RNA extract prepared from a particular cell or tissue source.

The above methods provide useful indirect evidence for determining codon preference. However, such indirect evidence may not provide an accurate indication of the translational efficiency of a given codon. Accordingly, there is a need to provide a method that more directly ascertains the translational efficiency of a codon in a cell or tissue.

SUMMARY OF THE INVENTION

In one aspect of the invention, there is provided a method for determining the translational efficiency of an individual codon in a cell, said method comprising:

- introducing into said cell a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of said individual codon, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide; and

- measuring expression of said reporter protein in said cell to determine the translational efficiency of said codon.

Preferably, the method further comprises comparing:

- expression of said reporter protein in a cell to which a synthetic construct comprising a tandem repeat of said individual codon was provided; and

- expression of said reporter protein in a cell to which a synthetic construct comprising a tandem repeat of another individual codon was provided;

to thereby determine the relative translational efficiency of said individual codons in said cell.

Suitably, the method further comprises comparing:

- expression of said reporter protein in a cell to which a synthetic construct comprising a tandem repeat of said individual codon was provided; and

- expression of said reporter protein in another cell to which a synthetic construct comprising a tandem repeat of said individual codon was provided;

to thereby determine the translational efficiency of said individual codon in said cell relative to said other cell.

Preferably, the method further comprises:

- introducing the synthetic construct into a progenitor cell of said cell; and

- producing said cell from said progenitor cell;

wherein said cell contains said synthetic construct.

Suitably, the method further comprises:

- introducing the synthetic construct into a progenitor of said cell; and

- growing an organism or part thereof from said progenitor cell;

wherein said organism comprises said cell containing said synthetic construct.

Suitably, the method further comprises:

- introducing the synthetic construct into an organism or part thereof such that said synthetic construct is introduced into said cell.

In another aspect, the invention resides in a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of individual codons, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide.

In yet another aspect of the invention, there is provided an improved method of constructing a synthetic polynucleotide from which a protein is selectively expressible in a target cell of an organism, relative to another cell of the organism, said method comprising:

- selecting a first codon of a parent polynucleotide for replacement with a synonymous codon which has a higher translational efficiency in said target cell than in said other cell; and

- replacing said first codon with said synonymous codon to form said synthetic polynucleotide, wherein said first codon and said synonymous codon are selected by:

- comparing translational efficiencies of individual codons in said target cell relative to said other cell using the method broadly described above; and

- selecting said first codon and said synonymous codon based on said comparison.

Preferably, said synonymous codon corresponds to a reporter construct from which the reporter protein is expressed in said target cell at a level that is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed from said reporter construct in said other cell.

In a further aspect, the invention provides an improved method of constructing a synthetic polynucleotide from which a protein is expressible in a target cell of an organism at a higher level than from a parent polynucleotide encoding said protein, said method comprising:

— selecting a first codon of the parent polynucleotide for replacement with a synonymous codon which has a higher translational efficiency in said target cell than said first codon;

— replacing said first codon with said synonymous codon to form said synthetic polynucleotide, wherein said first codon and said synonymous codon are selected by:

— comparing translational efficiencies of different individual codons in said target cell using the method broadly described above; and

— selecting said first codon and said synonymous codon based on said comparison.

Suitably, said synonymous codon corresponds to a reporter construct from which the reporter protein is expressed in said target cell at a level that is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed from the different reporter construct corresponding to said first codon.

DETAILED DESCRIPTION

1. Definitions

The articles "a" and "an" are used herein to refer to one or to more than one (i.e., to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

Throughout this specification, unless the context requires otherwise, the words "*comprise*", "*comprises*" and "*comprising*" will be understood to imply the inclusion of a stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements.

By "*expressible*" is meant expression of a protein to a level sufficient to effect a particular function associated with the protein. By contrast, the terms "*not expressible*" and "*not substantially expressible*" as used interchangeably herein refers to (a) no expression of a protein, (b) expression of a protein to a level that is not sufficient to effect a particular function associated with the protein, (c) expression of a protein, which cannot be detected by a monoclonal antibody specific for the protein, or (d) expression of a protein, which is less that 1% of the level expressed in a wild-type cell that normally expresses the protein.

By "*expressing said synthetic construct*" is meant transcribing the synthetic construct such that mRNA is produced.

By "*expression vector*" is meant any autonomous genetic element capable of directing the synthesis of a protein encoded by the vector. Such expression vectors are known by practitioners in the art.

As used herein, the term "function" refers to a biological, enzymatic, or therapeutic function.

By "*highly expressed genes*" is meant genes that express high levels of mRNA, and preferably high level of protein, relative to other genes.

By "*isoaccepting transfer RNA*" or "*iso-tRNA*" is meant one or more transfer RNA molecules that differ in their

anticodon nucleotide sequence but are specific for the same amino acid.

By "*natural gene*" is meant a gene that naturally encodes the protein. However, it is possible that the parent polynucleotide encodes a protein that is not naturally-occurring but has been engineered using recombinant techniques.

The term "*non-cycling cell*" as used herein refers to a cell that has withdrawn from the cell cycle and has entered the G0 state. In this state, it is known that transcription of endogenous genes and protein translation are at substantially reduced levels compared to phases of the cell cycle, namely G1, S, G2 and M. By contrast, the term "*cycling cell*" as used herein refers to a cell, which is in one of the above phases of the cell cycle.

By "*obtained from*" is meant that a sample such as, for example, a polynucleotide extract or polypeptide extract is isolated from, or derived from, a particular source of the host. For example, the extract can be obtained from a tissue or a biological fluid isolated directly from the host.

The term "*oligonucleotide*" as used herein refers to a polymer composed of a multiplicity of nucleotide residues (deoxyribonucleotides or ribonucleotides, or related structural variants or synthetic analogues thereof) linked via phosphodiester bonds (or related structural variants or synthetic analogues thereof). Thus, while the term "oligonucleotide" typically refers to a nucleotide polymer in which the nucleotide residues and linkages between them are naturally occurring, it will be understood that the term also includes within its scope various analogues including, but not restricted to, peptide nucleic acids (PNAs), phosphoramidates, phosphorothioates, methyl phosphonates, 2-O-methyl ribonucleic acids, and the like. The exact size of the molecule can vary depending on the particular

application. An oligonucleotide is typically rather short in length, generally from about 10 to 30 nucleotide residues, but the term can refer to molecules of any length, although the term "polynucleotide" or "nucleic acid" is typically used for large oligonucleotides.

By "*operably linked*" is meant that transcriptional and translational regulatory polynucleotides are positioned relative to a polypeptide-encoding polynucleotide in such a manner that the polynucleotide is transcribed and the polypeptide is translated.

By "*pharmaceutically-acceptable carrier*" is meant a solid or liquid filler, diluent or encapsulating substance that can be safely used in topical or systemic administration to a mammal.

"*Polypeptide*", "*peptide*" and "*protein*" are used interchangeably herein to refer to a polymer of amino acid residues and to variants and synthetic analogues of the same. Thus, these terms apply to amino acid polymers in which one or more amino acid residues is a synthetic non-naturally occurring amino acid, such as a chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally-occurring amino acid polymers.

The term "*polynucleotide*" or "*nucleic acid*" as used herein designates mRNA, RNA, cRNA, cDNA or DNA. The term typically refers to oligonucleotides greater than 30 nucleotide residues in length.

By "*primer*" is meant an oligonucleotide which, when paired with a strand of DNA, is capable of initiating the synthesis of a primer extension product in the presence of a suitable polymerizing agent. The primer is preferably single-stranded for maximum efficiency in amplification but can alternatively be double-stranded. A primer must be sufficiently long to prime the synthesis of extension products in the presence of the polymerization agent. The

length of the primer depends on many factors, including application, temperature to be employed, template reaction conditions, other reagents, and source of primers. For example, depending on the complexity of the target sequence,
5   the oligonucleotide primer typically contains 15 to 35 or more nucleotide residues, although it can contain fewer nucleotide residues. Primers can be large polynucleotides, such as from about 200 nucleotide residues to several kilobases or more. Primers can be selected to be
10 "substantially complementary" to the sequence on the template to which it is designed to hybridize and serve as a site for the initiation of synthesis. By "substantially complementary", it is meant that the primer is sufficiently complementary to hybridize with a target polynucleotide.
15 Preferably, the primer contains no mismatches with the template to which it is designed to hybridize but this is not essential. For example, non-complementary nucleotide residues can be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to
20 the template. Alternatively, non-complementary nucleotide residues or a stretch of non-complementary nucleotide residues can be interspersed into a primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridize therewith and thereby
25 form a template for synthesis of the extension product of the primer.

"Probe" refers to a molecule that binds to a specific sequence or sub-sequence or other moiety of another molecule. Unless otherwise indicated, the term "probe" typically refers
30 to a polynucleotide probe that binds to another polynucleotide, often called the "target polynucleotide", through complementary base pairing. Probes can bind target polynucleotides lacking complete sequence complementarity with the probe, depending on the stringency of the

hybridization conditions.   Probes can be labeled directly or indirectly.

The terms *"precursor cell or tissue"* and *"progenitor cell or tissue"* as used herein refer to a cell or tissue that can gives rise to a particular cell or tissue in which protein expression is to be targeted or in which translational efficiency of a codon is to be determined.

By *"recombinant polypeptide"* is meant a polypeptide made using recombinant techniques, *i.e.,* through the expression of a recombinant or synthetic polynucleotide.

"Stringency" as used herein, refers to the temperature and ionic strength conditions, and presence or absence of certain organic solvents, during hybridization.   The higher the stringency, the higher will be the degree of complementarity between immobilized polynucleotides and the labeled polynucleotide.

"Stringent conditions" refers to temperature and ionic conditions under which only polynucleotides having a high frequency of complementary bases will hybridize.   The stringency required is nucleotide sequence dependent and depends upon the various components present during hybridization.   Generally, stringent conditions are selected to be about 10 to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH.   The T_m is the temperature (under defined ionic strength and pH) at which 50% of a target sequence hybridizes to a complementary probe.

The term *"synthetic polynucleotide"* as used herein refers to a polynucleotide formed *in vitro* by the manipulation of a polynucleotide into a form not normally found in nature.   For example, the synthetic polynucleotide can be in the form of an expression vector.   Generally, such expression vectors include transcriptional and translational

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regulatory polynucleotide operably linked to the polynucleotide.

The term "*synonymous codon*" as used herein refers to a codon having a different nucleotide sequence than another codon but encoding the same amino acid as that other codon.

By "*translational efficiency*" is meant the efficiency of a cell's protein synthesis machinery to incorporate the amino acid encoded by a codon into a nascent polypeptide chain. This efficiency can be evidenced, for example, by the rate at which the cell is able to synthesize the polypeptide from an RNA template comprising the codon, or by the amount of the polypeptide synthesized from such a template.

By "*vector*" is meant a polynucleotide molecule, preferably a DNA molecule derived, for example, from a plasmid, bacteriophage, or plant virus, into which a polynucleotide can be inserted or cloned. A vector preferably contains one or more unique restriction sites and can be capable of autonomous replication in a defined host cell including a target cell or tissue or a progenitor cell or tissue thereof, or be integrable with the genome of the defined host such that the cloned sequence is reproducible. Accordingly, the vector can be an autonomously replicating vector, *i.e.*, a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, *e.g.*, a linear or closed circular plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector can contain any means for assuring self-replication. Alternatively, the vector can be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. A vector system can comprise a single vector or plasmid, two or more vectors or plasmids, which together contain the total DNA to be introduced into the genome of the host cell, or a

transposon. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. The vector can also include a selection marker such as an antibiotic resistance gene that can be used for selection of suitable transformants. Examples of such resistance genes are known to those of skill in the art and include the *nptII* gene that confers resistance to the antibiotics kanamycin and G418 (Geneticin®) and the *hph* gene which confers resistance to the antibiotic hygromycin B.

2. *Method of the invention*

The present invention is based, at least in part, on the discovery that different but synonymous stretches of identical codons fused respectively in frame with a reporter polynucleotide can give rise to different levels of reporter protein expressed within a given cell type. Not wishing to be bound by any particular theory, it is believed that a tandem series of identical codons causes a ribosome to pause during translation if the iso-tRNA corresponding to the identical codons is limiting. In this regard, it is known that ribosomal pausing leads to a failure to complete a nascent polypeptide chain and an uncoupling of transcription and translation. Accordingly, the levels of reporter protein expressed in the different cells or tissues are sensitive to the intracellular abundance of the iso-tRNA species corresponding to the identical codons and, therefore, provide a direct correlation of a cell's or tissue's preference for translating a given codon. This means, for example, that if the levels of the reporter protein obtained in a cell or tissue type to which a synthetic construct having a tandem series of identical first codons is provided are lower than the levels expressed in the same cell or tissue type to which a different synthetic construct having a tandem series of identical second codons is provided (*i.e.*, wherein the first

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codons are different from, but synonymous with, the second codons), then it can be deduced that the cell or tissue has a higher preference for the second codon relative to the first codon with respect to translation. Put another way, the second codon has a higher translational efficiency compared to the first codon in the cell or tissue type.

With regard to differential protein expression between different cell or tissue types, it will be appreciated that if the levels of the reporter protein obtained in a target cell or tissue type to which a synthetic construct having a tandem series of identical codons is provided are lower than the levels expressed in the another cell or tissue type to which the same synthetic construct is provided, then it can be deduced that the target cell or tissue has a higher preference for the codon relative to the other cell or tissue with respect to translation. Put another way, the codon has a higher translational efficiency in the target cell or tissue relative to the other cell or tissue type.

As used herein, expression of a protein in a tissue refers alternatively to expression of the protein within a cell of the tissue or production of the protein within a cell and export of the protein from the cell to, for example, the extracellular matrix of a tissue.

Suitably, the tandem repeat comprises at least three identical codons. Preferably, the tandem repeat comprises four identical codons, more preferably five or seven identical codons and most preferably six identical codons.

The tandem repeat can be fused at a location adjacent to, or within, the reporter polynucleotide. The location is preferably selected such that the tandem repeat interferes with translation of at least a detectable portion of the reporter protein such that expression of the protein can be detected or assessed. Preferably, the tandem repeat is

located immediately upstream (translationally) from the reporter polynucleotide.

It is of course possible that a tandem repeat of identical amino acid residues (*e.g.*, an oligo-proline repeat) can render the reporter protein unstable. Typically, protein instability is detected when expression of the reporter gene is not detectable with any choice of isoaccepting codon specific for the amino acid corresponding to the tandem repeat. The inventors have found in this regard that protein instability can be alleviated by use of at least one spacer codon within the tandem repeat of identical codons, wherein the spacer codon encodes a neutral amino acid.

The at least one spacer codon can be placed adjacent to, or interposed between, some or all of the identical codons corresponding to the tandem repeat. For example, a suitable interposition for a *penta*-repeat of identical codons can be selected from the group consisting of: (a) I-S-I-S-I-S-I-S-I-S; (b) S-I-S-I-S-I-S-I-S-I; (c) I-S-I-S-I-I-S-I; (d) I-S-I-I-S-I-S-I; (e) I-S-I-S-I-I-I; (f) I-I-S-I-S-I-I; (g) I-I-I-S-I-S-I; (h) I-S-I-I-S-I-I; (i) I-I-S-I-I-S-I; (j) I-S-I-I-I-S-I; (k) I-S-I-I-I-I; (l) I-I-S-I-I-I; (m) I-I-I-S-I-I; and (n) I-I-I-I-S-I, wherein I corresponds to an identical codon of a tandem repeat and S corresponds to a spacer codon.

Preferably, a spacer codon is efficiently translated in the cell or tissue type relative to other synonymous codons. This is important so that translation of the spacer codon is not rate limiting. The neutral amino acid includes, but is not restricted to, alanine and glycine.

The reporter polynucleotide can encode any suitable protein for which expression can be detected directly or indirectly such as by suitable assay. Suitable reporter polynucleotides include, but are not restricted to, polynucleotides encoding β-galactosidase, firefly luciferase, alkaline phosphatase, chloramphenicol acetyltransferase

(CAT), β-glucuronidase (GUS), herbicide resistance genes such as the bialophos resistance (BAR) gene that confers resistance to the herbicide BASTA, and green fluorescent protein (GFP). Assays for the activities associated with such proteins are known by those of skill in the art. Preferably, the reporter polynucleotide encodes GFP.

Persons of skill in the art will appreciate that reporter polynucleotides need not correspond to a full-length gene encoding a particular reporter protein. In this regard, the invention also contemplates reporter polynucleotide sub-sequences encoding desired portions of a parent reporter protein, wherein an activity or function of the parent protein is retained in said portions. A polynucleotide sub-sequence encodes a domain of the reporter protein having an activity associated therewith and preferably encodes at least 10, 20, 50, 100, 150, or 500 contiguous amino acid residues of the reporter protein.

The instant method is applicable to any suitable cell or tissue type and, hence, is not restricted to application to mammalian cells/tissues. Accordingly, the cell or tissue type can be of any animal or plant origin. The cell or tissue type can be of any suitable lineage. For example, a suitable cell can include a eukaryotic cell, and preferably a cell or cell line capable of being grown *in vitro*. Suitable cell lines can include, for example, CV-1 cells, COS cells, yeast or spodoptera cells. The invention also contemplates cells that can be prokaryotic in origin.

Suitable methods for isolating particular cells or tissues are known to those of skill in the art. For example, one can take advantage of one or more particular characteristics of a cell or tissue to specifically isolate the cell or tissue from a heterogeneous population. Such characteristics include, but are not limited to, anatomical location of a tissue, cell density, cell size, cell

morphology, cellular metabolic activity, cell uptake of ions such as Ca^{2+}, K^+, and H^+ ions, cell uptake of compounds such as stains, markers expressed on the cell surface, protein fluorescence, and membrane potential. Suitable methods that

5   can be used in this regard include surgical removal of tissue, flow cytometry techniques such as fluorescence-activated cell sorting (FACS), immunoaffinity separation (e.g., magnetic bead separation such as Dynabead™ separation), density separation (e.g., metrizamide, Percoll™,

10 or Ficoll™ gradient centrifugation), and cell-type specific density separation.

In an alternate embodiment, progenitor cells or tissues can be used for initially introducing the synthetic construct. Any suitable progenitor cell or tissue can be

15 used which gives rise to a particular cell or tissue of interest for which codon preference is to be ascertained. For example, a suitable progenitor cell can comprise an undifferentiated cell. In the case of a plant, a suitable progenitor cell and tissue can include a meristematic cell

20 and a callus tissue, respectively.

In another embodiment, the synthetic construct can be introduced first into an organism or part thereof before subsequent expression of the construct in a particular cell or tissue type. Any suitable organism is contemplated by the

25 invention including unicellular and as multi-cellular organisms. Exemplary multi-cellular organisms include plants and animals such as mammals (e.g., humans).

The invention further provides a synthetic construct comprising a reporter polynucleotide fused in frame with a

30 tandem repeat of (e.g., 2, 3, 4, 5, 6, or 7 or more) identical codons, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to one or more regulatory polynucleotides.

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The construction of the synthetic construct can be effected by any suitable technique. For example, *in vitro* mutagenesis methods can be employed, which are known to those of skill in the art. Suitable mutagenesis methods are described for example in the relevant sections of Ausubel, *et al.* (*supra*) and of Sambrook, *et al.*, (*supra*) which are incorporated herein by reference. Alternatively, suitable methods for altering DNA are set forth, for example, in U.S. Patent Nos. 4,184,917, 4,321,365 and 4,351,901, which are incorporated herein by reference. Instead of *in vitro* mutagenesis, the synthetic construct can be synthesized *de novo* using readily available machinery. Sequential synthesis of DNA is described, for example, in U.S. Patent No 4,293,652, which is incorporated herein by reference. However, it should be noted that the present invention is not dependent on, and not directed to, any one particular technique for constructing the synthetic construct.

Regulatory polynucleotides which can be utilized to regulate expression of the synthetic construct include, but are not limited to, a promoter, an enhancer, and a transcriptional terminator. Such regulatory polynucleotides are known to those of skill in the art. The construct preferably comprises at least one promoter. Suitable promoters that can be utilized to induce expression of the polynucleotides of the invention include constitutive promoters and inducible promoters.

The step of introducing the synthetic construct into a particular cell or tissue type, or into a progenitor cell or tissue thereof, or into an organism or part thereof for subsequent introduction into a particular cell or tissue will differ depending on the intended use and or species, and may involve lipofection, electroporation, micro-projectile bombardment infection by *Agrobacterium tumefaciens* or *A rhizogenes*, or protoplast fusion. Such methods are known to those skilled in the art.

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Alternatively, the step of introduction may involve non-viral and viral vectors, cationic liposomes, retroviruses and adenoviruses such as, for example, described in Mulligan, R.C., (1993 *Science* **260** 926-932) which is incorporated herein by reference. Such methods may include:

A. Local application of the synthetic nucleic acid sequence by injection (Wolff *et al.*, 1990, *Science* **247** 1465-1468, which is incorporated herein by reference), surgical implantation, instillation or any other means. This method may also be used in combination with local application by injection, surgical implantation, instillation or any other means, of cells responsive to the reporter protein encoded by the synthetic construct. This method may also be used in combination with local application by injection, surgical implantation, instillation or any other means, of another factor or factors required for the activity of said reporter protein.

B. General systemic delivery by injection of DNA, (Calabretta *et al.*, 1993, *Cancer Treat. Rev.* **19** 169-179, which is incorporated herein by reference), or RNA, alone or in combination with liposomes (Zhu *et al.*, 1993, *Science* **261** 209-212, which is incorporated herein by reference), viral capsids or nanoparticles (Bertling *et al.*, 1991, *Biotech. Appl. Biochem.* **13** 390-405, which is incorporated herein by reference) or any other mediator of delivery. Improved targeting might be achieved by linking the synthetic construct to a targeting molecule (the so-called "magic bullet" approach employing for example, an antibody), or by local application by injection, surgical implantation or any other means, of another factor or factors required for the activity of the protein produced from said synthetic construct, or of cells responsive to said reporter protein.

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C. Injection or implantation or delivery by any means, of cells that have been modified *ex vivo* by transfection (for example, in the presence of calcium phosphate: Chen *et al.*, 1987, *Mole. Cell Biochem.* **7** 2745-2752, or of cationic lipids and polyamines: Rose *et al.*, 1991, *BioTech.* **10** 520-525, which articles are incorporated herein by reference), infection, injection, electroporation (Shigekawa *et al.*, 1988, *BioTech.* **6** 742-751, which is incorporated herein by reference) or any other way so as to increase the expression of said synthetic construct in those cells. The modification may be mediated by plasmid, bacteriophage, cosmid, viral (such as adenoviral or retroviral; Mulligan, 1993, *Science* **260** 926-932; Miller, 1992, *Nature* **357** 455-460; Salmons *et al.*, 1993, *Hum. Gen. Ther.* **4** 129-141, which articles are incorporated herein by reference) or other vectors, or other agents of modification such as liposomes (Zhu *et al.*, 1993, *Science* **261** 209-212, which is incorporated herein by reference), viral capsids or nanoparticles (Bertling *et al.*, 1991, *Biotech. Appl. Biochem.* **13** 390-405, which is incorporated herein by reference), or any other mediator of modification. The use of cells as a delivery vehicle for genes or gene products has been described by Barr *et al.*, 1991, *Science* **254** 1507-1512 and by Dhawan *et al.*, 1991, *Science* **254** 1509-1512, which articles are incorporated herein by reference. Treated cells may be delivered in combination with any nutrient, growth factor, matrix or other agent that will promote their survival in the treated subject.

Advantageously, the translational efficiencies of different codons may be determined by comparing expression of the reporter protein in a given cell or tissue type or between different cell or tissue types. One of ordinary skill in the art will thereby be able to determine a "codon

preference table" for one or more cells or tissues. Comparison of codon preference tables relating to different cell or tissue types may be used to identify codons for tailoring a synthetic polynucleotide to target expression of a protein to a particular cell or tissue, as described hereinafter. Comparison of codons within a codon preference table for a particular cell or tissue type can be used to identify codons for tailoring a synthetic polynucleotide to express a protein at higher or lower levels in that cell or tissue type than a parent polynucleotide, as described hereinafter.

The invention further contemplates cells or tissues containing therein the synthetic construct of the invention, or alternatively, cells or tissues produced from the method of the invention.

3. Synthetic polynucleotides for targeting protein expression to a particular cell or tissue

The invention also provides an improved method of constructing a synthetic polynucleotide from which a protein is selectively expressible in a target cell of an organism, relative to another cell of the organism. This method is based in part on the method disclosed in copending International application PCT/AU98/00530 (the entire contents of which are hereby incorporated by reference) in which a first codon of a parent polynucleotide is replaced with a synonymous codon which has a higher translational efficiency in said target cell than in said other cell. The improved method of the invention is characterized by selecting the first and synonymous codons by comparing translational efficiencies of individual codons in said target cell relative to said other cell using the method broadly described is Section 2.

3.1. Selection of synonymous and first codons

The present method preferably includes the step of selecting the codons such that the synonymous codon has a higher translational efficiency in said target cell or tissue ("cell or tissue" is sometimes referred to herein as "cell/tissue") relative to said one or more other cells or tissues.

A method for determining translational efficiencies of different codons in and between different cells or tissues is described in detail in Section 2. The translational efficiencies so determined can be used to identify which isocoding triplets are differentially translated between the different cells or tissues. In a typical scenario, there will be: (A) codons with higher translational efficiencies in a target cell/tissue relative to one or more other cells/tissues; (B) codons with higher translational efficiencies in the one or more other cells/tissues relative to the target cell/tissue; and (C) codons with about the same translational efficiencies in the target cell/tissue relative to the one or more other cells/tissues. Synonymous codons are selected such that they correspond to (A) codons. Preferably, a synonymous codon is selected such that it has the largest difference in translational efficiency in the target cell or tissue relative to the existing codon (sometimes referred to as a "first codon") that it replaces. Existing codons in a parent polynucleotide are preferably selected such that they do not have the same translational bias as the synonymous codons with respect to the target cell/tissue and the one or more other cell/tissue (i.e., existing codons should preferably not correspond to (A) codons). However, existing codons can have similar translational efficiencies in each of the target cell/tissue and the one or more other cells/tissues (i.e., existing codons can correspond to (C) codons. They can also have a translational bias opposite to that of the synonymous codons

(*i.e.*, existing codons can, and preferably do, correspond to (B) codons).

Suitably, a synonymous codon has a translational efficiency in the target cell/tissue that is at least 110%, preferably at least 200%, more preferably at least 500%, and still more preferably at least 1000%, of that in the other cell(s)/tissue(s). In the case of two or more synonymous codons having similar translational efficiencies in the target cell/tissue relative to the other cell(s)/tissue(s), it will be appreciated that any one of these codons can be used to replace the existing codon.

It is preferable but not necessary to replace all the existing codons of the parent polynucleotide with synonymous codons having higher translational efficiencies in the target cell/tissue compared to the other cells/tissues. Increased expression can be accomplished even with partial replacement. Suitably, the replacement step affects 5%, 10%, 15%, 20%, 25%, 30%, more preferably 35%, 40%, 50%, 60%, 70% or more of the existing codons of the parent polynucleotide.

The difference in level of protein expressed in the target cell/tissue from a synthetic polynucleotide relative to that expressed in the other cell(s)/tissue(s) depends on the percentage of existing codons replaced by synonymous codons, and the difference in translational efficiencies of the synonymous codons in the target cell/tissue relative to the other cell(s)/tissue(s). Put another way, the fewer such replacements, and/or the smaller the difference in translational efficiencies of the synonymous between the different cells/tissues, the smaller the difference in protein expression between the target cell/tissue and the other cell(s)/tissue(s) will be. Conversely, the more such replacements, and/or the greater the difference in translational efficiencies of the synonymous codons between the different cells/tissues, the greater the difference in

protein expression between the target cell/tissue and the other cell(s)/tissue(s) will be. The inventors have found in this respect that a protein can be expressed from a synthetic polynucleotide in a target cell/tissue at levels greater than

5   10,000-fold over those expressed in another cell/tissue.

In a preferred embodiment, the synonymous codon is a codon which has a higher translational efficiency in the target cell or tissue relative to a precursor cell or tissue of the target cell or tissue.

10   In an alternate embodiment, the synonymous codon is a codon which has a higher translational efficiency in the target cell or tissue relative to a cell or tissue derived from said target cell or tissue.

The two codons can be selected by measuring
15   translational efficiencies of different codons in the target cell or tissue relative to the one or more other cells or tissues and identifying the at least one existing codon and the synonymous codon based on this measurement.

Suitably, the synonymous codon corresponds to a
20   reporter construct from which the reporter protein is expressed in said target cell at a level that is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed from the said reporter construct in said other cell.

25   *3.2. Construction of synthetic polynucleotides*

The step of replacing a synonymous codon for said first codon in a parent polynucleotide may be effected by any suitable technique. For example, *in vitro* mutagenesis methods may be employed as for example discussed in Section
30   2.

It is not necessary to replace all the first codons of the parent polynucleotide with synonymous codons each corresponding to a codon that has a higher translational

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efficiency in the target cell relative to said other cell. Increased expression may be accomplished even with partial replacement. Preferably, the replacing step affects 5%, 10%, 15%, 20%, 25%, 30%, more preferably 35%, 40%, 50%, 60%, 70% or more of the existing codons of the parent nucleic acid sequence.

The parent polynucleotide is preferably a natural gene.

The parent polynucleotide may be obtained from a plant or an animal. Alternatively, the parent polynucleotide may be obtained from any other eukaryotic organism or a prokaryotic organism. In a preferred embodiment, the parent polynucleotide is obtained from a pathogenic organism. In such a case, a natural host of the pathogenic organism is preferably a plant or animal. For example, the pathogenic organism may be a yeast, bacterium or virus. However, it will be understood that the parent polynucleotide need not be obtained from the organism in which a protein is to be expressed but may be obtained from any suitable source such as from another eukaryotic or prokaryotic organism.

Suitable proteins which may be used for selective expression in accordance with the invention include, but are not limited to the cystic fibrosis transmembrane conductance regulator (CFTR) protein, and adenosine deaminase (ADA). In the case of CFTR, a parent nucleic acid sequence encoding the CFTR protein which may be utilized to produce the synthetic nucleic acid sequence is described, for example, in Riordan et al (1989, *Science* **245** 1066-1073), and in the GenBank database under Accession No. HUMCFTRM, which are incorporated herein by reference.

Regulatory polynucleotides which may be utilized to regulate expression of the synthetic polynucleotide include, but are not limited to, a promoter, an enhancer, and a transcriptional terminator. Such regulatory polynucleotides are known to those of skill in the art. The construct

preferably comprises at least one promoter. Suitable promoters that can be utilized to induce expression of the synthetic polynucleotides of the invention include constitutive promoters and inducible promoters.

Synthetic polynucleotides according to the invention may be operably linked to one or more regulatory sequences in the form of an expression vector.

The invention also contemplates synthetic polynucleotides encoding one or more desired portions of the protein to be expressed. A polynucleotide encodes a domain of the protein having a function associated therewith, or which is otherwise detectable, and preferably encodes at least 10, 20, 50, 100, 150, or 500 contiguous amino acid residues of the protein.

4. Synthetic polynucleotides for enhanced protein expression in a particular cell or tissue

In contrast to differential protein expression between different cells/tissues, it will be appreciated that a synthetic polynucleotide may be tailored with synonymous codons such that expression of a protein in a target cell is enhanced. In this regard, the difference in level of protein expressed in the target cell/tissue from a synthetic polynucleotide relative to that expressed from a parent polynucleotide depends on the percentage of existing codons replaced by synonymous codons, and the difference in translational efficiencies between the existing codons and the synonymous codons in the target cell/tissue. Put another way, the fewer such replacements, and/or the smaller the difference in translational efficiencies between the synonymous and existing codons, the smaller the difference in protein expression between the synthetic polynucleotide and parent polynucleotide will be. Conversely, the more such replacements, and/or the greater the difference in

translational efficiencies between the synonymous and existing codons, the greater the difference in protein expression between the synthetic polynucleotide and parent polynucleotide will be. The inventors have found in this respect that a protein can be expressed from a synthetic polynucleotide in a target cell/tissue at levels greater than 10,000-fold than from a parent polynucleotide.

Preferably, the at least one existing codon and the synonymous codon are selected such that said protein is expressed from said synthetic polynucleotide in said target cell or tissue at a level which is at least 110%, preferably at least 200%, more preferably at least 500%, and most preferably at least 1000%, of that expressed from said parent polynucleotide in said target cell or tissue.

The invention is further described with reference to the following non-limiting examples.

EXAMPLE 1

Construction of expression vectors for determining relative codon preferences in mammalian cells.

Synthetic *gfp* genes were constructed in which a single artificial start codon (ATG) followed by a stretch of five identical codons is fused in frame immediately upstream of a *gfp* coding sequence. A reverse oligonucleotide primer (SEQ ID NO:185; sequence complementary to the termination codon for GFP, is underlined), and a suite of forward oligonucleotide primers (SEQ ID NO: 126 through 184; the first codon of GFP, is underlined) were synthesized and used for PCR amplification of a humanized *gfp* gene (SEQ ID NO:124) (GIBCO) as template with *Taq* DNA polymerase (Amplification parameters: 95°C/30 sec; 52°C/30 sec; 72°C/1 min; 30 cycles). The amplified fragments have nucleic acid sequences and

deduced amino acid sequences as shown in SEQ ID NO:1 through 124.

In summary, the synthetic fragments contain an artificial start codon followed by a tandem repeat of five identical codons specific for a given iso-tRNA species. The tandem repeat immediately precedes the second codon of the *gfp* gene. The synthetic fragments by SEQ ID NO, and encoded tandem repeat, are presented in the TABLE 1.

The amplified fragments were cloned between the *Eco*RI and *Kpn*I sites of the mammalian expression vector pCDNA3 containing SV40 *ori* (Invitrogen) and the CMV promoter.

Transfection of COS-1 cells

COS-1 cells were grown continuously in DMEM media supplemented with 10% fetal calf serum (FCS), glutamine, penicillin and streptomycin. Cells were passaged from a 150 cm^2 flask into multiple 25 cm^2 flasks. Cells were transfected using a QIAGEN Effectene™ transfection kit (and the manufacturer's instructions, incorporated herein by reference) when confluency of the cells was between 60-80%. Briefly, 1 µg of plasmid DNA was diluted into 10 µL of filtered TE buffer and 140 µL of QIAGEN™ Buffer EC. Eight microliters of QIAGEN™ Enhancer was added followed by vortexing and incubation at room temperature for 2-5 min. QIAGEN™ Effectene (10 µL) was added followed by vortexing for 10 seconds and a further incubation at room temperature for 10 min. The cells were washed once in 1x PBS followed by re-suspension in fresh media (1 mL). After 48 hrs, cells were harvested and washed in 1x PBA (phosphate buffered saline plus azide). Cells adhering to the flask were removed by scraping with a cell scraper. Cells were then filtered through a 70 µm filter before addition of 300 µL of 2% paraformaldehyde and 300 µL of 10x FCS. Cells were kept on ice in the dark until FACS analysis.

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Synthetic *gfp* mRNA expression of transfected cells was tested by reverse transcriptase PCR. GFP protein expression was analyzed by confocal microscopy and flow cytometry.

Confocal microscopy

Transfected COS-1 cells were examined using a Bio-Rad MRC-600 laser-scanning confocal microscope equipped with a krypton-argon laser and filter sets suitable for the detection of fluorescein and Texas red dyes (Bio-Rad K1yK2), and a Nikon 603 PlanApo™ numerical aperture 1.2 water-immersion objective. Dual-channel confocal images and video montages of the transfected cells can be suitably composed using ADOBE PhotoShop™.

Flow cytometry

Transfected COS-1 cells were analyzed with a Becton Dickinson™ Flow cytometer Elite II. Omega Filters™ allowed detection of green fluorescence emission (EMI510/20 — collects light from 490-530 nm) and yellow fluorescence emission (EM2 550/30 — collects light form 525-580 nm) from the transfected cells.

Results

A series of 64 reporter constructs (see TABLE 1) was made and validated, in which the *gfp* gene is preceded in frame by a tandem repeat of 5 identical codons. Together, the series covers the entire set of isoaccepting codon triplets.

The series was transfected into a single cell line, and expression levels measured by flow cytometry (see TABLE 2). Overall, the expression level of the reporter gene constructs in the cell line varied over a range of 20-fold, according to the triplet used in the reporter construct. Repeated determinations on the same construct showed excellent inter-assay reproducibility ($r^2 = 0.9$). Variation in expression

levels across the isoaccepting codons for a single amino acid ranged from 1.4-fold for valine to 13-fold for threonine, with a median of about 4-fold. Variation in expression between amino acids was of the same order of magnitude. The

5 order of magnitude of the effect is defined as an average of 4 fold per amino acid if 5 copies are incorporated, compatible with an extreme in range of expression levels of up to $(1.6)^{200} = 10^{86}$ over an average 200-amino acid residues protein. This figure is derived as:

10 **[1 + ((4-1)**(range of reporter construct expression)/

5 (no of triplets in the reporter construct))**]^{200}**(no of amino acid residues in the protein)

and is more than sufficient to explain the observed differences in expression of mammalian genes according to

15 codon usage.

The results presented in TABLE 2 also show that various codons in the undifferentiated epithelial cells (COS-1) have translational efficiencies at least two-fold higher or two-fold lower relative to those of their corresponding

20 synonymous codons. Representative codons having at least a two-fold higher translational efficiency relative to at least one of their corresponding synonymous codons include aga (Arg), cgg (Arg), tgc (Cys), gga (Gly), ggc (Gly), ccg (Pro), cga (Pro), aca (Thr), acg (Thr), and act (Thr). Thus, these

25 codons appear to be preferred for translation in the undifferentiated epithelial cells. By contrast, representative codons having at least a two-fold lower translational efficiency relative to at least one of their corresponding synonymous codons include agg (Arg), tgt (Cys),

30 ggg (Gly), ggt (Gly), ccc (Pro), cct (Pro), and acc (Thr). These latter codons would therefore appear to be less preferred for translation in the undifferentiated epithelial cells. Accordingly, if higher protein expression is required within undifferentiated epithelial cells such as COS-1 cells,

the preferred codons should be used to replace any existing codons of a parent polynucleotide encoding the protein that correspond to the less preferred codons. In this respect, a codon substitution algorithm for increasing protein expression in non-differentiated epithelial cells is presented in TABLE 3. However, if lower protein expression is required in non-differentiated epithelial cells, the less preferred codons should be used to replace any existing codons of the parent polynucleotide that correspond to the preferred codons.

The disclosure of every patent, patent application, and publication cited herein is hereby incorporated by reference in its entirety.

The present invention has been described in terms of particular embodiments found or proposed by the present inventors to comprise preferred modes for the practice of the invention. Those of skill in the art will appreciate that, in light of the present disclosure, numerous modifications and changes can be made in the particular embodiments exemplified without departing from the scope of the invention. All such modifications are intended to be included within the scope of the appended claims.

TABLE 1

Synthetic *gfp* constructs are tabulated by SEQ ID NO and by the codon corresponding to the tandem repeat of five identical codons immediately upstream of the *gfp* gene.

5   TABLE 2

Mean fluorescence intensities of up to four different samples of transiently transfected COS-1 cells are shown (Green mean 1-4). Synthetic *gfp* constructs are tabulated by SEQ ID NO and by the codon corresponding to the tandem repeat

10   immediately upstream of the *gfp* gene.

TABLE 3

Input codons and output codons represent, respectively, synonymous codons and existing (*i.e.*, "first") codons according to the invention. Change means an actual change of

15   a codon.

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<u>TABLES</u>

TABLE 1

Synthetic fragments and tandem repeats encoded thereby.

SEQ ID NO	Tandem repeat	SEQ ID NO	Tandem repeat
1	Ala (GCA) x 5	65	Leu (CTT) x 5
3	Ala (GCC) x 5	67	Leu (TTA) x 5
5	Ala (GCG) x 5	69	Leu (TTG) x 5
7	Ala (GCT) x 5	71	Lys (AAA) x 5
9	Arg (AGA) x 5	73	Lys (AAG) x 5
11	Arg (AGG) x 5	75	Phe (TTT) x 5
13	Arg (CGA) x 5	77	Phe (TTC) x 5
15	Arg (CGC) x 5	79	Pro (CCC) x 5
17	Arg (CGG) x 5	81	Pro (CCG) x 5
19	Arg (CGT) x 5	83	Pro (CCT) x 5
21	Asn (AAC) x 5	85	Pro (CGA) x 5
23	Asn (AAT) x 5	87	Ser (AGC) x 5
25	Asp (GAC) x 5	89	Ser (AGT) x 5
27	Asp (GAT) x 5	91	Ser (TCA) x 5
29	Cys (TGC) x 5	93	Ser (TCC) x 5
31	Cys (TGT) x 5	95	Ser (TCG) x 5
33	Gln (CAA) x 5	97	Ser (TCT) x 5
35	Gln (CAG) x 5	99	Thr (ACA) x 5
37	Gly (GAA) x 5	101	Thr (ACC) x 5
39	Gly (GAG) x 5	103	Thr (ACG) x 5
41	Gly (GGA) x 5	105	Thr (ACT) x 5

SEQ ID NO	Tandem repeat	SEQ ID NO	Tandem repeat
43	Gly (GGC) x 5	107	Trp (TGG) x 5
45	Gly (GGG) x 5	109	Tyr (TAT) x 5
47	Gly (GGT) x 5	111	Tyr (TAC) x 5
49	His (CAC) x 5	113	Val (GTA) x 5
51	His (CAT) x 5	115	Val (GTC) x 5
53	Ile (ATA) x 5	117	Val (GTG) x 5
55	Ile (ATC) x 5	119	Val (GTT) x 5
57	Ile (ATT) x 5	121	Stop (TAA) x 5
59	Leu (CTA) x 5	122	Stop (TAG) x 5
61	Leu (CTC) x 5	123	Stop (TGA) x 5
63	Leu (CTG) x 5	124	control

TABLE 2

GFP protein expression in transiently transfected COS-1 cells

SEQ ID NO	Codon	[DNA] (µg/mL)	Green mean 1	Green mean 2	Green mean 3	Green mean 4	Average
1	Ala (GCA)	1.07	45.70	54.40			50.05
3	Ala (GCC)	1.10	43.70	50.00			46.85
5	Ala (GCG)	0.03	28.50	42.40			35.45
7	Ala (GCT)	0.56	11.60	48.30			29.95
9	Arg (AGA)	0.90	29.00	33.00			31.00
11	Arg (AGG)	0.34	7.35	2.88			5.12
13	Arg (CGA)	1.00	18.30	14.20			16.25
15	Arg (CGC)	0.86	14.60	16.00			15.30
17	Arg (CGG)	1.00	22.50	20.60			21.55
19	Arg (CGT)	0.68	21.70	32.20			26.95
21	Asn (AAC)	0.02					
23	Asn (AAT)	0.38	28.30	8.22			18.26
25	Asp (GAC)	0.46	24.90	17.80			21.35
27	Asp (GAT)	1.39	14.50	18.90			16.70
29	Cys (TGC)	0.68	21.90	16.10			19.00
31	Cys (TGT)	1.14	5.95	5.89			5.92
33	Gln (CAA)	0.28	26.50	43.50			35.00
35	Gln (CAG)	1.98	44.70	48.60			46.65
37	Glu (GAA)	0.60	10.30	22.70			16.50
39	Glu (GAG)	0.43	3.86				
41	Gly (GGA)	0.33	28.80	36.30			32.55
43	Gly (GGC)	1.62	17.80	28.10			22.95
45	Gly (GGG)	1.15	6.43	4.96			5.70
47	Gly (GGT)	1.39	7.12	4.02			5.57
49	His (CAC)	1.62	29.90	39.70			34.80
51	His (CAT)	1.69	43.40	37.20			40.30
53	Ile (ATA)	0.69	2.76	3.98			3.37

SEQ ID NO	Codon	[DNA] (µg/mL)	Green mean 1	Green mean 2	Green mean 3	Green mean 4	Average
55	Ile (ATC)	1.52	4.12	2.83			3.48
57	Ile (ATT)	1.77	3.19	3.16			3.18
59	Leu (CTA)	0.10	15.00	3.01	5.26	2.44	6.43
61	Leu (CTC)	1.74	2.70	2.92	2.56		2.73
63	Leu (CTG)	0.41	2.80	7.51	2.63		4.31
65	Leu (CTT)	1.43	3.17	3.56	2.70		3.14
67	Leu (TTA)	0.62	3.85	3.91	2.66		3.47
69	Leu (TTG)	0.70	2.87	4.63	2.85		3.45
71	Lys (AAA)	0.10	11.90	8.24			10.07
73	Lys (AAG)	0.56	19.20	16.00			17.60
75	Phe (TTT)	2.28	2.67				
77	Phe (TTC)	1.65	4.35				
79	Pro (CCC)	0.40	12.00	8.95			10.48
81	Pro (CCG)	0.13	17.40	25.40			21.40
83	Pro (CCT)	0.40	10.60	9.89			10.25
85	Pro (CGA)	0.17	27.20	34.80			31.00
87	Ser (AGC)	0.03	62.40				
89	Ser (AGT)	0.81	23.10				
91	Ser (TCA)	0.08	30.70	37.20			33.95
93	Ser (TCC)	1.68	32.90				
95	Ser (TCG)	1.58	60.00				
97	Ser (TCT)	0.62	26.80	40.70			33.75
99	Thr (ACA)	1.70	37.80	39.90			38.85
101	Thr (ACC)	7.69	3.48	2.75			3.12
103	Thr (ACG)	1.06	36.10	44.10			40.10
105	Thr (ACT)	1.42	38.80	42.60			40.70
107	Trp (TGG)	1.19	5.21	4.29			4.75
109	Tyr (TAT)	0.02					
111	Tyr (TAC)	1.07	12.00	15.00			13.50
113	Val (GTA)	0.16	10.50	3.81			7.16
115	Val (GTC)	0.66	15.20	4.55	3.65	5.06	7.12
117	Val (GTG)	0.10	9.17	4.29	7.03	2.36	5.71

SEQ ID NO	Codon	[DNA] (µg/mL)	Green mean 1	Green mean 2	Green mean 3	Green mean 4	Average
119	Val (GTT)	0.49	14.10	2.63	3.70	2.49	5.73
121	stop (TAA)	1.88	39.40	35.30			37.35
122	stop (TAG)	2.86	2.88	3.28			3.08
123	stop (TGA)	0.02					
124			9.34	61.60	30.40	55.00	39.09
GFP alone control			2.33	2.21	2.16	2.00	2.18

TABLE 3

Substitution algorithm used for high level expression in non-differentiated epithelial cells

Input Codon	Output Codon	Amino Acid	Change
AAA	AAG	LYS	Yes
AAC	AAC	ASN	No
AAG	AAG	LYS	No
AAT	AAC	ASN	Yes
AAU	AAC	ASN	Yes
ACA	ACC	THR	Yes
ACC	ACC	THR	No
ACG	ACC	THR	Yes
ACT	ACC	THR	Yes
ACU	ACC	THR	Yes
AGA	AGG	ARG	Yes
AGC	AGC	SER	No
AGG	AGG	ARG	No
AGT	AGC	SER	Yes
AGU	AGC	SER	Yes
ATA	ATC	ILE	Yes
ATC	ATC	ILE	No
ATG	ATG	MET	No
ATT	ATC	ILE	Yes
AUA	ATC	ILE	Yes
AUC	ATC	ILE	No
AUG	ATG	MET	No
AUU	ATC	ILE	Yes
CAA	CAG	GLN	Yes
CAC	CAC	HIS	No
CAG	CAG	GLN	No
CAT	CAC	HIS	Yes
CAU	CAC	HIS	Yes
CCA	CCC	PRO	Yes
CCC	CCC	PRO	No
CCG	CCC	PRO	Yes
CCT	CCC	PRO	Yes
CCU	CCC	PRO	Yes
CGA	CGC	ARG	Yes

Input Codon	Output Codon	Amino Acid	Change
CGC	CGC	ARG	No
CGG	CGC	ARG	Yes
CGT	CGC	ARG	Yes
CGU	CGC	ARG	Yes
CTA	CTG	LEU	Yes
CTC	CTG	LEU	Yes
CTG	CTG	LEU	No
CTT	CTG	LEU	Yes
CUA	CTG	LEU	Yes
CUC	CTG	LEU	Yes
CUG	CTG	LEU	No
CUU	CTG	LEU	Yes
GAA	GAG	GLU	Yes
GAC	GAC	ASP	No
GAG	GAG	GLU	No
GAT	GAC	ASP	Yes
GAU	GAC	ASP	Yes
GCA	GCC	ALA	Yes
GCC	GCC	ALA	No
GCG	GCC	ALA	Yes
GCT	GCC	ALA	Yes
GCU	GCC	ALA	Yes
GGA	GGC	GLY	Yes
GGC	GGC	GLY	No
GGG	GGG	GLY	No
GGT	GGC	GLY	Yes
GGU	GGC	GLY	Yes
GTA	GTG	VAL	Yes
GTC	GTG	VAL	Yes
GTG	GTG	VAL	No
GTT	GTG	VAL	Yes
GUA	GTG	VAL	Yes
GUC	GTG	VAL	Yes
GUG	GTG	VAL	No
GUU	GTG	VAL	Yes
TAA	TAA	XXX	No
TAC	TAC	TYR	No
TAG	TAG	XXX	No
TAT	TAC	TYR	Yes
TCA	TCC	SER	Yes

Input Codon	Output Codon	Amino Acid	Change
TCC	TCC	SER	No
TCG	TCC	SER	Yes
TCT	TCC	SER	Yes
TGA	TGA	XXX	No
TGC	TGC	CYS	No
TGG	TGG	TRP	No
TGT	TGT	CYS	No
TTA	CTG	LEU	Yes
TTC	TTC	PHE	No
TTG	CTG	LEU	Yes
TTT	TTC	PHE	No
UAA	TAA	XXX	No
UAC	TAC	TYR	No
UAG	TAG	XXX	No
UAU	TAC	TYR	Yes
UCA	TCC	SER	Yes
UCC	TCC	SER	No
UCG	TCC	SER	Yes
UCU	TCC	SER	Yes
UGA	TGA	XXX	No
UGC	TGC	CYS	No
UGG	TGG	TRP	No
UGU	TGT	CYS	No
UUA	CTG	LEU	Yes
UUC	TTC	PHE	No
UUG	CTG	LEU	Yes
UUU	TTC	PHE	Yes

WHAT IS CLAIMED IS:

1. A method for determining the translational efficiency of an individual codon in a cell, said method comprising:

- introducing into said cell a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of said individual codon, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide; and

- measuring expression of said reporter protein in said cell to determine the translational efficiency of said codon.

2. The method of claim 1, further comprising comparing:

- expression of said reporter protein in a cell to which a synthetic construct comprising a tandem repeat of said individual codon was provided; and

- expression of said reporter protein in a cell to which a synthetic construct comprising a tandem repeat of another individual codon was provided;

to thereby determine the relative translational efficiency of said individual codons in said cell.

3. The method of claim 1, further comprising comparing:

- expression of said reporter protein in a cell to which a synthetic construct comprising a tandem repeat of said individual codon was provided; and

- expression of said reporter protein in another cell to which a synthetic construct comprising a tandem repeat of said individual codon was provided;

to thereby determine the translational efficiency of said individual codon in said cell relative to said other cell.

4. The method of claim 1, further comprising:

     - introducing the synthetic construct into a progenitor
cell of said cell; and

     - producing said cell from said progenitor cell;

wherein said cell contains said synthetic construct.

5. The method of claim 1, further comprising

     - introducing the synthetic construct into a progenitor
of said cell; and

     - growing an organism or part thereof from said
progenitor cell;

wherein said organism comprises said cell containing said
synthetic construct.

6. The method of claim 1, further comprising

     - introducing the synthetic construct into an organism
or part thereof such that said synthetic construct is
introduced into said cell.

7. A synthetic construct comprising a reporter
polynucleotide fused in frame with a tandem repeat of
individual codons, wherein said reporter polynucleotide
encodes a reporter protein, and wherein said synthetic
construct is operably linked to a regulatory polynucleotide.

8. A vector comprising the synthetic construct of claim 7.

9. A cell comprising the synthetic construct of claim 7.

10. A cell comprising the vector of claim 9.

11. An improved method of constructing a synthetic
polynucleotide from which a protein is selectively
expressible in a target cell of an organism, relative to
another cell of the organism, said method comprising:

     - selecting a first codon of a parent polynucleotide
for replacement with a synonymous codon which has a higher

translational efficiency in said target cell than in said other cell; and

- replacing said first codon with said synonymous codon to form said synthetic polynucleotide, wherein said first codon and said synonymous codon are selected by:

- comparing translational efficiencies of individual codons in said target cell relative to said other cell; and

- selecting said first codon and said synonymous codon based on said comparison, wherein said comparison comprises;

- introducing into said target cell and said other cell a synthetic construct comprising a reporter polynucleotide fused in frame with a tandem repeat of an individual codon, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide; and

- comparing expression of said reporter protein in said target cell relative to said other cell;

to thereby determine the translation efficiency of individual codons in said target cell relative to said other cell.

12. The method of claim 11, wherein said synonymous codon corresponds to a reporter construct from which the reporter protein is expressed in said target cell at a level that is at least 110% of that expressed from the said reporter construct in said other cell.

13. An improved method of constructing a synthetic polynucleotide from which a protein is expressible in a target cell of an organism at a higher level than from a parent polynucleotide expressing said protein, said method comprising:

- 44 -

- selecting a first codon of the parent polynucleotide for replacement with a synonymous codon which has a higher translational efficiency in said target cell than said first codon;

5   - replacing said first codon with said synonymous codon to form said synthetic polynucleotide, wherein said first codon and said synonymous codon are selected by:

- comparing translational efficiencies of different individual codons in said target cell; and

10   - selecting said first codon and said synonymous codon based on said comparison wherein said comparison comprises:

- introducing into a target cell a synthetic construct comprising a reporter polynucleotide fused in

15   frame with a tandem repeat of an individual codon, wherein said reporter polynucleotide encodes a reporter protein, and wherein said synthetic construct is operably linked to a regulatory polynucleotide;

- introducing into a target cell a different

20   synthetic construct comprising the reporter polynucleotide fused in frame with a tandem repeat of another individual codon; and

- comparing expression of said reporter protein from each synthetic construct in said target cell;

25   to thereby determine the translation efficiency of individual codons in said target cell.

14. The method of claim 13, wherein said synonymous codon corresponds to a reporter construct from which the reporter protein is expressed in said target cell at a level that is

30   at least 110% of that expressed from the different reporter construct corresponding to said first codon.

15. A synthetic polynucleotide constructed according to the method of claim 11 or claim 13.

16. A vector comprising the synthetic polynucleotide of claim 15.

17. A cell comprising the synthetic polynucleotide of claim 15.

18. A cell comprising the vector of claim 16.

SEQUENCE LISTING

<110> The University of Queensland (all designated States except US)
      Frazer, Ian Hector and Zhou, Jian (US only)

<120> METHOD AND POLYNUCLEOTIDES FOR DETERMINING TRANSLATIONAL
      EFFICIENCY OF A CODON

<130> Codon optimization

<140> Not yet assigned
<141> Herewith

<150> PP8078
<151> 1999-01-08

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<170> PatentIn Ver. 2.0

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 1   5   10   15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20   25   30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35   40   45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50   55   60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65   70   75   80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
               100   105   110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384

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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
    115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac      432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac      480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att      528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca      576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc      672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                       732
Leu Tyr Lys
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
    115                 120                 125
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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130   135   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                 165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

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  1   5   10   15

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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                 20   25   30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35   40   45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50   55   60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85   90   95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys

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                  100                      105                      110
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc      384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac      432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac      480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att      528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca      576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc      672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110
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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
    115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
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Leu Tyr Lys
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Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc  288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95
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tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
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cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
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Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
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Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
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Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
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Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
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Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
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Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
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Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
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Leu Tyr Lys
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tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80
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gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                     732
Leu Tyr Lys
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Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80
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Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
             85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
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<210> 9
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(AGA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 9
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atg aga aga aga aga aga agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1           5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
```

```
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                    85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 10
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 10
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60
```

```
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
             85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
         100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
         115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150                 155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
             165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
         195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys
```

```
<210> 11
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(AGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 11
atg agg agg agg agg agg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5               10              15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20              25              30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35              40              45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
```

```
                50                        55                        60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                      70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                            85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                    165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys


<210> 12
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 12
Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5               10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45
```

```
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60
```

```
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80
```

```
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95
```

```
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
        100             105             110
```

```
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125
```

```
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140
```

```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160
```

```
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175
```

```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
        180             185             190
```

```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

```
Leu Tyr Lys
```

```
<210> 13
<211> 732
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Arg(CGA)5GFP
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<220>
<221> CDS
<222> (1)..(732)
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```
<400> 13
atg cga cga cga cga cga agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45
```

```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65              70              75              80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
             85              90              95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
         115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                 165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 14
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 14
```
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20              25              30
```

```
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35          40                  45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55                  60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70                  75                  80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
Leu Tyr Lys
```

```
<210> 15
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 15
atg cgc cgc cgc cgc cgc agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc      144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca      192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca      240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc      288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag      336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc      384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
         115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac      432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac      480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att      528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                 165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca      576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
         195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc      672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                      732
Leu Tyr Lys
```

<210> 16
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 16
```
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15
```

```
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
        20               25               30
```

```
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35               40               45
```

```
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50               55               60
```

```
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65               70               75               80
```

```
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85               90               95
```

```
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
        100              105              110
```

```
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115              120              125
```

```
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130              135              140
```

```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145              150              155              160
```

```
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165              170              175
```

```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
        180              185              190
```

```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195              200              205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210              215              220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225              230              235              240
```

```
Leu Tyr Lys
```

<210> 17
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 17
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atg cgg cgg cgg cgg cgg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5               10              15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
```

```
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20           25               30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35           40               45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50               55               60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65               70               75               80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85               90               95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100              105              110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115              120              125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130              135              140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145              150              155              160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165              170              175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180              185              190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195              200              205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210              215              220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225              230              235              240

ctg tac aag tga                                                   732
Leu Tyr Lys
```

```
<210> 18
<211> 243
<212> PRT
<213> Artificial Sequence
```

<400> 18

```
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 19
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 19
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atg cgt cgt cgt cgt cgt agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
```

```
      1                5                    10                     15

 gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
 Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

 tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
 Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45

 ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
 Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60

 ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
 Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

 gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
 Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                  90                  95

 tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
 Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100                 105                 110

 acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
 Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115                 120                 125

 gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
 Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
             130                 135                 140

 aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
 Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
 145                 150                 155                 160

 aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
 Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165                 170                 175

 gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
 Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180                 185                 190

 atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
 Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195                 200                 205

 cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
 Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
 210                 215                 220

 ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
 Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225                 230                 235                 240

 ctg tac aag tga                                                    732
 Leu Tyr Lys
```

```
<210> 20
<211> 243
```

<212> PRT
<213> Artificial Sequence

<400> 20

```
Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                10                15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys
```

<210> 21
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asn(AAC)5GFP

<220>
<221> CDS
<222> (1)..(732)

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<400> 21
atg aac aac aac aac aac agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                     732
Leu Tyr Lys
```

<210> 22
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 22
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1   5   10   15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20   25   30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35   40   45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50   55   60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   105   110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115   120   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130   135   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 23
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asn(AAT)5GFP

<220>

<221> CDS
<222> (1)..(732)

<400> 23

```
atg aat aat aat aat aat agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Asn Asn Asn Asn Asn Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

732

ctg tac aag tga
Leu Tyr Lys

<210> 24
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 24

Met	Asn	Asn	Asn	Asn	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val
1				5				10					15	

| Val | Pro | Ile | Leu | Val | Glu | Leu | Asp | Gly | Asp | Val | Asn | Gly | His | Lys | Phe |
| | | 20 | | | | | 25 | | | | | 30 | | |

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35   40   45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50   55   60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
               85   90   95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
          100   105   110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
     115   120   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130   135   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
               165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
          180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
          195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 25
<211> 732
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Asp(GAC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 25
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atg gac gac gac gac agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt  96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc 144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca 192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca 240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc 288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag 336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc 384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac 432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac 480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att 528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca 576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc 624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc 672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag 720
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230             235                 240
```

```
ctg tac aag tga                                                   732
Leu Tyr Lys
```

```
<210> 26
<211> 243
<212> PRT
<213> Artificial Sequence
```

```
<400> 26
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys
```

```
<210> 27
<211> 732
<212> DNA
```

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asp(GAT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 27

```
atg gat gat gat gat gat agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Asp Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
               100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
           115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
   130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
               180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
           195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
```

```
              210                    215.                 220
      ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
      Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
      225                 230                 235                 240

      ctg tac aag tga                                                    732
      Leu Tyr Lys
```

```
<210> 28
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 28
Met Asp Asp Asp Asp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

```
<210> 29
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cys(TGC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 29
atg tgc tgc tgc tgc tgc agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc      144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca      192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca      240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc      288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag      336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc      384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac      432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac      480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att      528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca      576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205
```

```
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 30
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 30

```
Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

Leu Tyr Lys

```
<210> 31
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cys(TGT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 31
atg tgt tgt tgt tgt tgt agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190
```

```
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag     720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                     732
Leu Tyr Lys
```

<210> 32
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 32

```
Met Cys Cys Cys Cys Cys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5              10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220
```

```
     Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
     225                 230                 235                 240

     Leu Tyr Lys


     <210> 33
     <211> 732
     <212> DNA
     <213> Artificial Sequence

     <220>
     <223> Description of Artificial Sequence: Gln(CAA)5GFP

     <220>
     <221> CDS
     <222> (1)..(732)

     <400> 33
     atg caa caa caa caa caa agc aag ggc gag gaa ctg ttc act ggc gtg      48
     Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
      1               5                  10                  15

     gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
     Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                 20                  25                  30

     tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
     Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45

     ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
     Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
         50                  55                  60

     ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
     Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
     65                  70                  75                  80

     gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
     Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                  90                  95

     tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
     Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                 100                 105                 110

     acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
     Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115                 120                 125

     gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
     Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
         130                 135                 140

     aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
     Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
     145                 150                 155                 160

     aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
     Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165                 170                 175

     gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
```

```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc      672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                      732
Leu Tyr Lys
```

<210> 34
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 34
```
Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5              10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230             235                 240
```

```
Leu Tyr Lys
```

<210> 35
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gln(CAG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 35

```
atg cag cag cag cag cag agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45
```

```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
         50                  55                  60
```

```
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80
```

```
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95
```

```
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110
```

```
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125
```

```
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140
```

```
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160
```

```
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
```

```
                165                    170                    175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
        180             185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210             215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys


<210> 36
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 36
Met Gln Gln Gln Gln Gln Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190
```

```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210             215             220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

```
Leu Tyr Lys
```

```
<210> 37
<211> 732
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Glu(GAA)5GFP
```

```
<220>
<221> CDS
<222> (1)..(732)
```

```
<400> 37
atg gaa gaa gaa gaa agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5               10              15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt  96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc  288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag  336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
        100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc  384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac  432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac  480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160
```

```
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys


<210> 38
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 38
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175
```

```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 39
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Glu(GAG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 39

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atg gag gag gag gag gag agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140
```

```
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                   732
Leu Tyr Lys
```

```
<210> 40
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 40
Met Glu Glu Glu Glu Glu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
         130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160
```

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 41
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 41
atg gga gga gga gga gga agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1   5   10   15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20   25   30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35   40   45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50   55   60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100   105   110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115   120   125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432

```
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac       480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att       528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca       576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc       624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc       672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag       720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                       732
Leu Tyr Lys


<210> 42
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 42
Met Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1             5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140
```

```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145               150               155               160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165               170               175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180               185               190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195               200               205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210               215               220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225               230               235               240

Leu Tyr Lys
```

```
<210> 43
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 43
atg ggc ggc ggc ggc ggc agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
```

```
              115                      120                      125
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                     135                     140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                     150                     155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                     170                     175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                     185                     190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                     200                     205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                     215                     220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                     230                     235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 44
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 44
Met Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
    115                 120                 125
```

```
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
Leu Tyr Lys
```

```
<210> 45
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 45
atg ggg ggg ggg ggg ggg agc aag ggc gag gaa ctg ttc act ggc gtg     48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5              10                      15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
              20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50                  55                  60

ctc gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                    85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110
```

```
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 46
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 46
Met Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110
```

```
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125
```

```
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130             135             140
```

```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160
```

```
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175
```

```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190
```

```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210             215             220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

```
Leu Tyr Lys
```


```
<210> 47
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 47
atg ggt ggt ggt ggt ggt agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Gly Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5               10              15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95
```

```
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100          ·          105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
·Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                   732
Leu Tyr Lys
```

```
<210> 48
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 48
Met Gly Gly Gly Gly Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95
```

```
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
         100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
         115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                 165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys
```

```
<210> 49
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 49
atg cac cac cac cac cac agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1           5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
```

```
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys


<210> 50
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 50
Met His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80
```

```
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys
```

<210> 51
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAT)5GFP

<220>
<221> CDS
<222> (1)..(732)

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<400> 51
atg cat cat cat cat cat agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met His His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5              10              15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20              25              30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35              40              45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
```

```
          65                     70                     75                     80
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                     90                     95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                    105                    110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                    120                    125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                    135                    140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                    150                    155                    160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165                    170                    175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                    185                    190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                    200                    205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                    215                    220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                    230                    235                    240

ctg tac aag tga                                                   732
Leu Tyr Lys
```

```
<210> 52
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 52
Met His His His His Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5               10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55                  60
```

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   105   110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115   120   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130   135   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 53
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 53
atg ata ata ata ata ata agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1   5   10   15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20   25   30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35   40   45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50   55   60

```
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 54
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 54
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45
```

```
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60
```

```
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80
```

```
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95
```

```
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
        100             105             110
```

```
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125
```

```
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140
```

```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160
```

```
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175
```

```
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
        180             185             190
```

```
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240
```

```
Leu Tyr Lys
```

```
<210> 55
<211> 732
<212> DNA
<213> Artificial Sequence
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```
<220>
<223> Description of Artificial Sequence: Ile(ATC)5GFP
```

```
<220>
<221> CDS
<222> (1)..(732)
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```
<400> 55
atg atc atc atc atc atc agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1           5              10              15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45
```

```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65              70              75              80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
             85              90              95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
         100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
     115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
             165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
         180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
         195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag     720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                      732
Leu Tyr Lys


<210> 56
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 56
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1              5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20              25              30
```

```
Ser  Val  Ser  Gly  Glu  Gly  Glu  Gly  Asp  Ala  Thr  Tyr  Gly  Lys  Leu  Thr
          35                  40                  45

Leu  Lys  Phe  Ile  Cys  Thr  Thr  Gly  Lys  Leu  Pro  Val  Pro  Trp  Pro  Thr
          50                  55                  60

Leu  Val  Thr  Thr  Phe  Ser  Tyr  Gly  Val  Gln  Cys  Phe  Ser  Arg  Tyr  Pro
65                  70                  75                                  80

Asp  His  Met  Lys  Gln  His  Asp  Phe  Phe  Lys  Ser  Ala  Met  Pro  Glu  Gly
                    85                  90                  95

Tyr  Val  Gln  Glu  Arg  Thr  Ile  Phe  Phe  Lys  Asp  Asp  Gly  Asn  Tyr  Lys
               100                 105                 110

Thr  Arg  Ala  Glu  Val  Lys  Phe  Glu  Gly  Asp  Thr  Leu  Val  Asn  Arg  Ile
          115                 120                 125

Glu  Leu  Lys  Gly  Ile  Asp  Phe  Lys  Glu  Asp  Gly  Asn  Ile  Leu  Gly  His
     130                 135                 140

Lys  Leu  Glu  Tyr  Asn  Tyr  Asn  Ser  His  Asn  Val  Tyr  Ile  Met  Ala  Asp
145                 150                 155                                 160

Lys  Gln  Lys  Asn  Gly  Ile  Lys  Val  Asn  Phe  Lys  Ile  Arg  His  Asn  Ile
               165                 170                 175

Glu  Asp  Gly  Ser  Val  Gln  Leu  Ala  Asp  His  Tyr  Gln  Gln  Asn  Thr  Pro
               180                 185                 190

Ile  Gly  Asp  Gly  Pro  Val  Leu  Leu  Pro  Asp  Asn  His  Tyr  Leu  Ser  Thr
          195                 200                 205

Gln  Ser  Ala  Leu  Ser  Lys  Asp  Pro  Asn  Glu  Lys  Arg  Asp  His  Met  Val
     210                 215                 220

Leu  Leu  Glu  Phe  Val  Thr  Ala  Ala  Gly  Ile  Thr  His  Gly  Met  Asp  Glu
225                 230                 235                                 240

Leu  Tyr  Lys
```

<210> 57
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 57

```
atg att att att att att agc aag ggc gag gaa ctg ttc act ggc gtg     48
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
```

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35   40   45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50   55   60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
              85   90   95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   105   110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
           115   120   125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
      130   135   140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
             165   170   175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
          180   185   190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
          195   200   205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
      210   215   220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

ctg tac aag tga   732
Leu Tyr Lys

<210> 58
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 58
Met Ile Ile Ile Ile Ile Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
   1   5   10   15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
        20   25   30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35   40   45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50   55   60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   105   110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115   120   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130   135   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 59
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 59
atg cta cta cta cta cta agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1   5   10   15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe

```
                        20                      25                      30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc        144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                      40                      45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca        192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                      55                      60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca        240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                      70                      75                      80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc        288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85                      90                      95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag        336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                     105                     110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc        384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                     120                     125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac        432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                     135                     140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac        480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                     150                     155                     160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att        528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                     170                     175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca        576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                     185                     190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc        624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                     200                     205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc        672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                     215                     220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag        720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                     230                     235                     240

ctg tac aag tga                                                        732
Leu Tyr Lys
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<210> 60
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 60

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Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                10                15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                25                30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                40                45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                55                60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                70                75                80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85                90                95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100               105               110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115               120               125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130               135               140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145               150               155               160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165               170               175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180               185               190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195               200               205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210               215               220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225               230               235               240

Leu Tyr Lys


<210> 61
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 61
atg ctc ctc ctc ctc ctc agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                10                15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
         20              25              30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc  144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35              40              45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca  192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca  240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc  288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
             85              90              95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag  336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
         100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc  384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
         115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac  432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac  480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att  528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
             165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca  576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
         180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc  624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
         195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc  672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag  720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                  732
Leu Tyr Lys
```

```
<210> 62
<211> 243
<212> PRT
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<213> Artificial Sequence

<400> 62

| Met
1 | Leu | Leu | Leu | Leu
5 | Leu | Ser | Lys | Gly | Glu
10 | Glu | Leu | Phe | Thr | Gly
15 | Val |

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
          20   25   30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35   40   45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50   55   60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
              100   105   110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115   120   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130   135   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
              165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
              180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 63
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 63

- lxv -

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atg ctg ctg ctg ctg ctg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                   732
Leu Tyr Lys
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<210> 64
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 64
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1   5   10   15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20   25   30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35   40   45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50   55   60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   105   110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115   120   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130   135   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 65
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTT)5GFP

<220>
<221> CDS

<222> (1)..(732)

<400> 65

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atg ctt ctt ctt ctt ctt agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                 20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

Leu Tyr Lys

<210> 66
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 66

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Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```


<210> 67
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(TTA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 67
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atg tta tta tta tta tta agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
```

225   230   235   240

ctg tac aag tga   732
Leu Tyr Lys

<210> 68
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 68
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1   5   10   15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20   25   30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35   40   45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50   55   60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   105   110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115   120   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130   135   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 69
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(TTG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 69
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atg ttg ttg ttg ttg ttg agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
              20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                  85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
         115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                 165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
         195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc     672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210                 215                 220
```

```
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                     732
Leu Tyr Lys
```

<210> 70
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 70

```
Met Leu Leu Leu Leu Leu Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
    115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys
```

<210> 71

```
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 71
atg aaa aaa aaa aaa aaa agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc     624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205
```

```
cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 72
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 72
```
Met Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
        100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
    115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
    195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

Leu Tyr Lys
```

```
<210> 73
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 73
atg aag aag aag aag aag agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Lys Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
```

```
            Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                 200                 205

            cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
            Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                 215                 220

            ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
            Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
            225                 230                 235                 240

            ctg tac aag tga                                                    732
            Leu Tyr Lys
```

<210> 74
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 74

```
            Met Lys Lys Lys Lys Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
            1               5                   10                  15

            Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                        20                  25                  30

            Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                    35                  40                  45

            Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                50                  55                  60

            Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
            65                  70                  75                  80

            Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                            85                  90                  95

            Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                        100                 105                 110

            Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                        115                 120                 125

            Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                130                 135                 140

            Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
            145                 150                 155                 160

            Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                            165                 170                 175

            Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                        180                 185                 190

            Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                        195                 200                 205

            Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210                 215                 220

            Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
```

```
        225                 230                 235                 240

        Leu Tyr Lys


        <210> 75
        <211> 732
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Description of Artificial Sequence: Phe(TTT)5GFP

        <220>
        <221> CDS
        <222> (1)..(732)

        <400> 75
        atg ttt ttt ttt ttt ttt agc aag ggc gag gaa ctg ttc act ggc gtg     48
        Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
          1               5                  10                  15

        gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
        Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                     20                  25                  30

        tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
        Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                 35                  40                  45

        ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
        Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
             50                  55                  60

        ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
        Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
         65                  70                  75                  80

        gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
        Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                         85                  90                  95

        tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
        Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                    100                 105                 110

        acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
        Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115                 120                 125

        gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
        Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                 135                 140

        aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
        Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
        145                 150                 155                 160

        aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
        Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                        165                 170                 175

        gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
        Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
```

```
                 180                    185                    190
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195              200              205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210              215              220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225              230              235              240

ctg tac aag tga                                                   732
Leu Tyr Lys
```

<210> 76
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 76
```
Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
```

```
            210                    215                    220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

```
Leu Tyr Lys
```

```
<210> 77
<211> 732
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Description of Artificial Sequence: Phe(TTC)5GFP
```

```
<220>
<221> CDS
<222> (1)..(732)
```

```
<400> 77
atg ttc ttc ttc ttc ttc agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1           5                  10                  15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45
```

```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60
```

```
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80
```

```
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                  90                  95
```

```
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110
```

```
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125
```

```
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140
```

```
aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160
```

```
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175
```

```
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca      576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc      672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                      732
Leu Tyr Lys


<210> 78
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 78
Met Phe Phe Phe Phe Phe Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
```

                195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 79
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 79
atg ccc ccc ccc ccc ccc agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1   5   10   15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20   25   30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35   40   45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50   55   60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65   70   75   80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85   90   95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100   105   110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115   120   125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130   135   140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

```
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 80
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 80
Met Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
 '          20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
```

```
                 180                    185                    190
    Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195                    200                    205

    Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
         210                    215                    220

    Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
    225                    230                    235                    240

    Leu Tyr Lys
```

```
<210> 81
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 81
atg ccg ccg ccg ccg ccg agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
```

```
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 82
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 82
Met Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
            85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
```

```
              165                  170                  175
```

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 83
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CCT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 83
atg cct cct cct cct cct agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1   5   10   15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
              20   25   30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
          35   40   45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
      50   55   60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                  85   90   95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
              100   105   110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
          115   120   125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
```

```
              130                    135                    140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                   732
Leu Tyr Lys


<210> 84
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 84
Met Pro Pro Pro Pro Pro Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5               10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
```

```
      145                    150                    155                    160
```

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                   165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
          180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
          195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

```
<210> 85
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Pro(CGA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 85
atg cga cga cga cga cga agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Arg Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125
```

```
gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 86
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 86
```
Met Arg Arg Arg Arg Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
        20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
```

```
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

```
<210> 87
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(AGC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 87
atg agc agc agc agc agc agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                   40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110
```

```
acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                   732
Leu Tyr Lys
```

```
<210> 88
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 88
Met Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
```

```
             115                   120                   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

```
<210> 89
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(AGT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 89
atg agt agt agt agt agt agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
```

```
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
        100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                   732
Leu Tyr Lys
```

```
<210> 90
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 90
Met Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
```

```
                    100                      105                      110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
        210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

```
<210> 91
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(TCA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 91
atg tca tca tca tca tca agc aag ggc gag gaa ctg ttc act ggc gtg       48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt       96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc      144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca      192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca      240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc      288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
```

```
                    85                      90                      95
tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag      336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                     105                     110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc      384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                     120                     125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac      432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                     135                     140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac      480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                     150                     155                     160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att      528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                    165                     170                     175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca      576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                    180                     185                     190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                    195                     200                     205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc      672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                    210                     215                     220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                     230                     235                     240

ctg tac aag tga                                                      732
Leu Tyr Lys
```

```
<210> 92
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 92
Met Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
```

```
                85                       90                       95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                     105                     110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                     120                     125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
            130                     135                     140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                     150                     155                     160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                     170                     175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                     185                     190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                     200                     205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
            210                     215                     220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                     230                     235                     240

Leu Tyr Lys
```

```
<210> 93
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(TCC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 93
atg tcc tcc tcc tcc tcc agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80
```

```
gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                      90                      95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                     105                     110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                     120                     125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                     135                     140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                     150                     155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                     170                     175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                     185                     190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                     200                     205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                     215                     220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                     230                     235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 94
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 94
Met Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
```

```
        65                        70                     75                      80
       Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85                     90                      95

       Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                       100                    105                     110

       Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                   115                    120                    125

       Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
           130                    135                    140

       Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
       145                    150                    155                    160

       Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                       165                    170                    175

       Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                   180                    185                    190

       Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                   195                    200                    205

       Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
           210                    215                    220

       Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
       225                    230                    235                    240

       Leu Tyr Lys
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<210> 95
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(TCG)5GFP

<220>
<221> CDS
<222> (1)..(732)

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<400> 95
atg tcg tcg tcg tcg tcg agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60
```

```
ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65              70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 96
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 96
Met Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
```

```
              50                    55                    60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                    70                    75                    80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                      85                    90                    95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
             100                   105                   110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115                   120                   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
             130                   135                   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                   150                   155                   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                   170                   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180                   185                   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195                   200                   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210                   215                   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                   230                   235                   240

Leu Tyr Lys


<210> 97
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ser(TCT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 97
atg tct tct tct tct tct agc aag ggc gag gaa ctg ttc act ggc gtg     48
Met Ser Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                 20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
```

```
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                        85              90              95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

<210> 98
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 98

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Met Ser Ser Ser Ser Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
```

```
                35                        40                        45
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                115                 120                 125
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180                 185                 190
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195                 200                 205
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
Leu Tyr Lys
```

```
<210> 99
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thr(ACA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 99
atg aca aca aca aca aca agc aag ggc gag gaa ctg ttc act ggc gtg     48
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
```

```
                35                          40                          45

  ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
  Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
       50                      55                      60

  ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
  Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
   65                      70                      75              80

  gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
  Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                   85                      90                      95

  tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
  Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                  100                     105                     110

  acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
  Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
              115                     120                     125

  gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
  Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
          130                     135                     140

  aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
  Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
  145                     150                     155                 160

  aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
  Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                      165                     170                     175

  gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
  Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                  180                     185                     190

  atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
  Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
              195                     200                     205

  cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
  Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
          210                     215                     220

  ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
  Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
  225                     230                     235                 240

  ctg tac aag tga                                                    732
  Leu Tyr Lys
```

```
<210> 100
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 100
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
```

```
                 20                     25                      30
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50              55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70                  75                      80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp·His Tyr Gln Gln Asn Thr Pro
                180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 101
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thr(ACC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 101

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atg acc acc acc acc acc agc aag ggc gag gaa ctg ttc act ggc gtg     48
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt     96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30
```

```
tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40                      45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50              55                      60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65          70                      75                      80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

                                                                   732
ctg tac aag tga
Leu Tyr Lys
```

<210> 102
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 102
Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val

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                1                    5                        10                        15
              Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                          20                  25                      30

              Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                          35                  40                      45

              Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
                  50                  55                      60

              Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
              65                  70                      75                      80

              Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                          85                  90                      95

              Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                          100                 105                     110

              Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
                          115                 120                     125

              Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
                          130                 135                     140

              Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
              145                 150                     155                     160

              Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                          165                 170                     175

              Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                          180                 185                     190

              Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                          195                 200                     205

              Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                  210                 215                     220

              Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
              225                 230                     235                     240

              Leu Tyr Lys


              <210> 103
              <211> 732
              <212> DNA
              <213> Artificial Sequence

              <220>
              <223> Description of Artificial Sequence: Thr(ACG)5GFP

              <220>
              <221> CDS
              <222> (1)..(732)

              <400> 103
              atg acg acg acg acg acg agc aag ggc gag gaa ctg ttc act ggc gtg     48
              Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
                1               5                   10                      15
```

```
gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

                                                                  732
ctg tac aag tga
Leu Tyr Lys


<210> 104
<211> 243
<212> PRT
<213> Artificial Sequence
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<400> 104
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Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 105
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Thr(ACT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 105
atg act act act act act agc aag ggc gag gaa ctg ttc act ggc gtg   48

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        Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
         1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt       96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                 20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc      144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
             35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca      192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
         50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca      240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc      288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag      336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc      384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
             115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac      432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
         130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac      480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att      528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                     165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca      576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
             180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
             195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc      672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
         210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

                                                                     732
ctg tac aag tga
Leu Tyr Lys
```

<210> 106

<211> 243
<212> PRT
<213> Artificial Sequence

<400> 106

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Met Thr Thr Thr Thr Thr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 107
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Trp(TGG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 107

atg tgg tgg tgg tgg tgg agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Trp Trp Trp Trp Trp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1   5   10   15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20   25   30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35   40   45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50   55   60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   105   110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115   120   125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130   135   140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165   170   175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195   200   205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210   215   220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

  732
ctg tac aag tga
Leu Tyr Lys

<210> 108
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 108
Met Trp Trp Trp Trp Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1   5   10   15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20   25   30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35   40   45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50   55   60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65   70   75   80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   105   110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115   120   125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
     130   135   140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165   170   175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195   200   205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
     210   215   220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225   230   235   240

Leu Tyr Lys

<210> 109
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Tyr(TAT)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 109
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atg tat tat tat tat tat agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

```
ctg tac aag tga
Leu Tyr Lys
```

<210> 110
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 110

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Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 111
<211> 732
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Tyr(TAC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 111
atg tac tac tac tac tac agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220
```

```
ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235                 240

                                                                    732
ctg tac aag tga
Leu Tyr Lys
```

<210> 112
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 112

```
Met Tyr Tyr Tyr Tyr Tyr Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5               10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235                 240

Leu Tyr Lys
```

<210> 113
<211> 732

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTA)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 113

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atg gta gta gta gta agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
           100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
       115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
   130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
               165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
               180                 185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
       195                 200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

                                                                     732
ctg tac aag tga
Leu Tyr Lys


<210> 114
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 114
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys
```

<210> 115
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTC)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 115
atg gtc gtc gtc gtc gtc agc aag ggc gag gaa ctg ttc act ggc gtg   48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1   5   10   15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt   96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20   25   30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35   40   45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
50   55   60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65   70   75   80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85   90   95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100   105   110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115   120   125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130   135   140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145   150   155   160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165   170   175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca   576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180   185   190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc   624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr

```
              195                    200                       205
    cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc   672
    Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                     215                 220

    ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag   720
    Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
    225                     230                 235                240
                                                                      732
    ctg tac aag tga
    Leu Tyr Lys
```

<210> 116
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 116

```
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
1               5                   10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50                  55                  60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                 200                 205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                 215                 220

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

Leu Tyr Lys

<210> 117
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTG)5GFP

<220>
<221> CDS
<222> (1)..(732)

<400> 117

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atg gtg gtg gtg gtg gtg agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                 85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att     528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca     576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                 185                 190
```

```
atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
 225             230             235             240

                                                                   732
ctg tac aag tga
Leu Tyr Lys
```

<210> 118
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 118
```
Met Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1.                  5               10                  15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90                  95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

Leu Tyr Lys


<210> 119
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Val(GTT)5GFP

<220>
<221> CDS
<222> (1)..(732)


<400> 119
atg gtt gtt gtt gtt gtt agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met Val Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                  10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
             20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc   144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
         35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca   192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
     50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca   240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc   288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                     85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag   336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc   384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac   432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac   480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att   528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                 170                 175
```

```
gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185                 190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200                 205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215                 220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240

                                                                   732
ctg tac aag tga
Leu Tyr Lys
```

```
<210> 120
<211> 243
<212> PRT
<213> Artificial Sequence

<400> 120
Met Val Val Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
 1           5               10              15

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20              25              30

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35              40              45

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
    115             120             125

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
            165             170             175

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
            195             200             205
```

```
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
210             215                 220
```

```
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230                 235                 240
```

```
Leu Tyr Lys
```

```
<210> 121
<211> 732
<212> DNA
<213> Artificial Sequence
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```
<220>
<223> Description of Artificial Sequence: Stop(TAA)5GFP
```

```
<220>
<221> CDS
<222> (1)..(732)
```

```
<400> 121
atg taa taa taa taa taa agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met                     Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1             5                     10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
            35                  40                  45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca     192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                  60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca     240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65                  70                  75                  80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc     288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                  95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag     336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
                100                 105                 110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc     384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
            115                 120                 125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac     432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
        130                 135                 140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac     480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                 150                 155                 160
```

```
aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170                175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
                180             185                190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
                195             200                205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
                210             215                220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                 230             235                240

ctg tac aag tga                                                    732
Leu Tyr Lys
```

```
<210> 122
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Stop(TAG)5GFP

<220>
<221> CDS
<222> (1)..(732)


<400> 122
atg tag tag tag tag tag agc aag ggc gag gaa ctg ttc act ggc gtg    48
Met                     Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1             5                   10                15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt    96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
                20                  25                30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc    144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
                35                  40                45

ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
        50                  55                60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
 65                 70                  75                80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85                  90                95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
```

```
              100                      105                      110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc      384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115                  120                  125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac      432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130                  135                  140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac      480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145                  150                  155                  160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att      528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165                  170                  175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca      576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180                  185                  190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc      624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195                  200                  205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc      672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210                  215                  220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag      720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225                  230                  235                  240

ctg tac aag tga                                                      732
Leu Tyr Lys


<210> 123
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Stop(TGA)5GFP

<220>
<221> CDS
<222> (1)..(732)


<400> 123
atg tga tga tga tga tga agc aag ggc gag gaa ctg ttc act ggc gtg      48
Met                     Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
  1               5                   10                  15

gtc cca att ctc gtg gaa ctg gat ggc gat gtg aat ggg cac aaa ttt      96
Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
            20                  25                  30

tct gtc agc gga gag ggt gaa ggt gat gcc aca tac gga aag ctc acc     144
Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
        35                  40                  45
```

```
ctg aaa ttc atc tgc acc act gga aag ctc cct gtg cca tgg cca aca    192
Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
    50              55              60

ctg gtc act acc ttc tct tat ggc gtg cag tgc ttt tcc aga tac cca    240
Leu Val Thr Thr Phe Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro
65              70              75              80

gac cat atg aag cag cat gac ttt ttc aag agc gcc atg ccc gag ggc    288
Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
                85              90              95

tat gtg cag gag aga acc atc ttt ttc aaa gat gac ggg aac tac aag    336
Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
            100             105             110

acc cgc gct gaa gtc aag ttc gaa ggt gac acc ctg gtg aat aga atc    384
Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
        115             120             125

gag ctg aag ggc att gac ttt aag gag gat gga aac att ctc ggc cac    432
Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
    130             135             140

aag ctg gaa tac aac tat aac tcc cac aat gtg tac atc atg gcc gac    480
Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
145             150             155             160

aag caa aag aat ggc atc aag gtc aac ttc aag atc aga cac aac att    528
Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
                165             170             175

gag gat gga tcc gtg cag ctg gcc gac cat tat caa cag aac act cca    576
Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
            180             185             190

atc ggc gac ggc cct gtg ctc ctc cca gac aac cat tac ctg tcc acc    624
Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr
        195             200             205

cag tct gcc ctg tct aaa gat ccc aac gaa aag aga gac cac atg gtc    672
Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
    210             215             220

ctg ctg gag ttt gtg acc gct gct ggg atc aca cat ggc atg gac gag    720
Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu
225             230             235             240

                                                                    732
ctg tac aag tga
Leu Tyr Lys
```

```
<210> 124
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: GFP humanized
      control

<220>
<221> CDS
<222> (1)..(717)
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<400> 124

```
atg agc aag ggc gag gaa ctg ttc act ggc gtg gtc cca att ctc gtg      48
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
 1               5                  10                  15

gaa ctg gat ggc gat gtg aat ggg cac aaa ttt tct gtc agc gga gag      96
Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
             20                  25                  30

ggt gaa ggt gat gcc aca tac gga aag ctc acc ctg aaa ttc atc tgc     144
Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
         35                  40                  45

acc act gga aag ctc cct gtg cca tgg cca aca ctg gtc act acc ttc     192
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
     50                  55                  60

tct tat ggc gtg cag tgc ttt tcc aga tac cca gac cat atg aag cag     240
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65                  70                  75                  80

cat gac ttt ttc aag agc gcc atg ccc gag ggc tat gtg cag gag aga     288
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                 85                  90                  95

acc atc ttt ttc aaa gat gac ggg aac tac aag acc cgc gct gaa gtc     336
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
             100                 105                 110

aag ttc gaa ggt gac acc ctg gtg aat aga atc gag ctg aag ggc att     384
Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
         115                 120                 125

gac ttt aag gag gat gga aac att ctc ggc cac aag ctg gaa tac aac     432
Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
     130                 135                 140

tat aac tcc cac aat gtg tac atc atg gcc gac aag caa aag aat ggc     480
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145                 150                 155                 160

atc aag gtc aac ttc aag atc aga cac aac att gag gat gga tcc gtg     528
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                 165                 170                 175

cag ctg gcc gac cat tat caa cag aac act cca atc ggc gac ggc cct     576
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
             180                 185                 190

gtg ctc ctc cca gac aac cat tac ctg tcc acc cag tct gcc ctg tct     624
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
         195                 200                 205

aaa gat ccc aac gaa aag aga gac cac atg gtc ctg ctg gag ttt gtg     672
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
     210                 215                 220

acc gct gct ggg atc aca cat ggc atg gac gag ctg tac aag tga        717
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225                 230                 235
```

<210> 125

<211> 238
<212> PRT
<213> Artificial Sequence

<400> 125
Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1   5   10   15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
            20   25   30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
        35   40   45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
    50   55   60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65   70   75   80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
                85   90   95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
            100   105   110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
        115   120   125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
    130   135   140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145   150   155   160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
                165   170   175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
            180   185   190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
        195   200   205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
    210   215   220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
225   230   235

<210> 126
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCA)5
      primer

<400> 126
cggggtacca tggcagcagc agcagcaagc aaggCgagg aactgttcac tggc   54

```
<210> 127
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCC)5
      primer

<400> 127
cggggtacca tggccgccgc cgccgccagc aagggcgagg aactgttcac tggc          54


<210> 128
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCG)5
      primer

<400> 128
cggggtacca tggcggcggc ggcggcgagc aagggcgagg aactgttcac tggc          54


<210> 1293
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ala(GCT)5
      primer

<400> 129
cggggtacca tggctgctgc tgctgctagc aagggcgagg aactgttcac tggc          54


<210> 130
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(AGA)5
      primer

<400> 130
cggggtacca tgagaagaag aagaagaagc aagggcgagg aactgttcac tggc          54


<210> 131
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(AGG)5
      primer

<400> 131
cggggtacca tgaggaggag gaggaggagc aagggcgagg aactgttcac tggc          54
```

<210> 132
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGA)5
      primer

<400> 132
cggggtacca tgcgacgacg acgacgaagc aagggcgagg aactgttcac tggc   54

<210> 133
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGC)5
      primer

<400> 133
cggggtacca tgcgccgccg ccgccgcagc aagggcgagg aactgttcac tggc   54

<210> 134
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Arg(CGG)5
      primer

<400> 134
cggggtacca tgcggcggcg gcggcggagc aagggcgagg aactgttcac tggc   54

<210> 135
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: arg(CGT)5
      primer

<400> 135
cggggtacca tgcgtcgtcg tcgtcgtagc aagggcgagg aactgttcac tggc   54

<210> 136
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asn(AAC)5
      primer

<400> 136
cggggtacca tgaacaacaa caacaacagc aagggcgagg aactgttcac tggc   54

<210> 137
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asn(AAT)5
      primer

<400> 137
cggggtacca tgaataataa taataatagc aagggcgagg aactgttcac tggc   54

<210> 138
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asp(GAC)5
      primer

<400> 138
cggggtacca tggacgacga cgacgacagc aagggcgagg aactgttcac tggc   54

<210> 139
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Asp(GAT)5
      primer

<400> 139
cggggtacca tggatgatga tgatgatagc aagggcgagg aactgttcac tggc   54

<210> 140
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cys(TGC)5
      primer

<400> 140
cggggtacca tgtgctgctg ctgctgcagc aagggcgagg aactgttcac tggc   54

<210> 141
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cys(TGT)5
      primer

<400> 141

cggggtacca tgtgttgttg ttgttgt<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 142
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gln(CAA)5
      primer

<400> 142
cggggtacca tgcaacaaca acaacaa<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 143
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gln(CAG)5
      primer

<400> 143
cggggtacca tgcagcagca gcagcag<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 144
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Glu(GAA)5
      primer

<400> 144
cggggtacca tggaagaaga agaagaa<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 145
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Glu(GAG)5
      primer

<400> 145
cggggtacca tggaggagga ggaggag<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 146
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGA)5
      primer

```
<400> 146
cggggtacca tgggaggagg aggaggaagc aagggcgagg aactgttcac tggc          54


<210> 147
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGC)5
      primer

<400> 147
cggggtacca tgggcggcgg cggcggcagc aagggcgagg aactgttcac tggc          54


<210> 148
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGG)5
      primer

<400> 148
cggggtacca tgggggggggg gggggggagc aagggcgagg aactgttcac tggc         54


<210> 149
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Gly(GGT)5
      primer

<400> 149
cggggtacca tgggtggtgg tggtggtagc aagggcgagg aactgttcac tggc          54


<210> 150
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAC)5
      primer

<400> 150
cggggtacca tgcaccacca ccaccacagc aagggcgagg aactgttcac tggc          54


<210> 151
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: His(CAT)5
      primer
```

<400> 151
cggggtacca tgcatcatca tcatcat<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 152
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATA)5
     primer

<400> 152
cggggtacca tgataataat aataata<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 153
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATC)5
     primer

<400> 153
cggggtacca tgatcatcat catcatc<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 154
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ile(ATT)5
     primer

<400> 154
cggggtacca tgattattat tattatt<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 155
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTA)5
     primer

<400> 155
cggggtacca tgctactact actacta<u>agc</u> aagggcgagg aactgttcac tggc   54

<210> 156
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTC)5

primer

<400> 156
cggggtacca tgctcctcct cctcctcagc aagggcgagg aactgttcac tggc   54

<210> 157
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTG)5
      primer

<400> 157
cggggtacca tgctgctgct gctgctgagc aagggcgagg aactgttcac tggc   54

<210> 158
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(CTT)5
      primer

<400> 158
cggggtacca tgcttcttct tcttcttagc aagggcgagg aactgttcac tggc   54

<210> 159
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(TTA)5
      primer

<400> 159
cggggtacca tgttattatt attattaagc aagggcgagg aactgttcac tggc   54

<210> 160
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Leu(TTG)5
      primer

<400> 160
cggggtacca tgttgttgtt gttgttgagc aagggcgagg aactgttcac tggc   54

<210> 161
<211> 54
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Lys(AAA)5
     primer

<400> 161
cggggtacca tgaaaaaaaa aaaaaaaagc aagggcgagg aactgttcac tggc   54

<210> 162
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Lys(AAG)5
     primer

<400> 162
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<210> 1726
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<210> 182
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<210> 183
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<220>
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<212> DNA
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      oligonucleotide common primer

<400> 185
ccggaattct cacttgtaca ggtggtccat gcc        33
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International application No.

PCT/AU 00/00008

A.	CLASSIFICATION OF SUBJECT MATTER

Int Cl^7:   C12Q 1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B.	FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
AS ABOVE

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
AS BELOW

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
CA, Medline, Biosis, WPID
Codon (bias/preference/use/usage/efficiency); tandem repeat; reporter

C.	DOCUMENTS CONSIDERED TO BE RELEVANT	
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	Kurland, GC. N Codon Bias and Gene Expression. FEBS Letters. 1991. 285(2):165-169	All
A	Sharp PM et al. Codon usage: mutational bias, translational selection, or both? Biochem Soc Trans 1993. 21(4):835-41	All
A	AU 56657/96. BIOGEN MV. 9/10/86	All

	Further documents are listed in the continuation of Box C	X	See patent family annex

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance		
"E"	earlier application or patent but published on or after the international filing date	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
7 February 2000	1 8 FEB 2000

Name and mailing address of the ISA/AU	Authorized officer
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This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report	Patent Family Member
AU 56657/96	WO 86/05810
	EP 215110
	US 5242811

END OF ANNEX